

Art Unit: 1652

## APPENDIX A

AF106851  
 LOCUS AF106851 2816 bp DNA linear BCT 08-APR-1999  
 DEFINITION *Staphylococcus aureus* LytN (lytN) and FmhC (fmhC) genes, complete cds.  
 ACCESSION AF106851  
 VERSION AF106851.1 GI:4574236  
 KEYWORDS  
 SOURCE *Staphylococcus aureus*  
 ORGANISM *Staphylococcus aureus*  
 Bacteria; Firmicutes; Bacillales; *Staphylococcus*.  
 REFERENCE 1 (bases 1 to 2816)  
 AUTHORS Tschierske,M., Mori,C., Rohrer,S., Ehrlert,K., Shaw,K.J. and Berger-Bachi,B.  
 TITLE Identification of three additional femAB-like open reading frames in *Staphylococcus aureus*  
 JOURNAL FEMS Microbiol. Lett. 171 (2), 97-102 (1999)  
 MEDLINE 99177558  
 PUBMED 10077832  
 REFERENCE 2 (bases 1 to 2816)  
 AUTHORS Shaw,K.J.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-NOV-1998) Chemotherapy and Molecular Genetics, Schering-Plough Research Institute, 2015 Galloping Hill Road 4700, Kenilworth, NJ 07033, USA  
 FEATURES Location/Qualifiers  
 source 1. .2816  
 /organism="Staphylococcus aureus"  
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 /db\_xref="ATCC:55748"  
 /db\_xref="taxon:1280"  
 gene 193. .1344  
 /gene="lytN"  
 CDS 193. .1344  
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 NYFGYYSFREAPKTQIYTVKKGDTLSAIALKYKTTVSNIQNTNNIANPNLFIGQKLK  
 VPMTPLVEPKPKTVSSNNKNSNSSTINYLKTLENRGWDFDGSYGWQCFDLVNVYWNH  
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 /codon\_start=1  
 /transl\_table=11  
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 FILVDPYLIENLRDANGRIIKNYNNNSVIVKMLKGIGYLHQGYTTGYSNKSQIRWISVL  
 DLKDKDENQLLKEMEYQTRRNKKTIEIGVKVEDLSIETNRFYKLFQMAECKHGFF  
 MNEDYFJKLMKQEIYKDKAMLKIAICINLNEYQDKLKIQLLKIEENEMMTVNRALNENPNSK"

Art Unit: 1652

RNKSKLNQLNMQLSSINNRISKTEELILEDGPVLDLAAALFICTDDEVYYLSSGSNPK  
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ORIGIN

Alignment Scores:

Pred. No.:	1.1e-147	Length:	2816
Score:	2176.00	Matches:	414
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-09-932-474-1 (1-414) x AF106851 (1-2816)

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Qy 21 HisTyrThrGlnSerIleGluLeuTyrAsnTyrArgAsnLysIleAsnHisGluAlaHis 40  
 Db 1432 CATTATACACAGTCTATAGAATTATATAATTAGAAATAAAATCATGAAGCACAT 1491

Qy 41 IleValGlyValLysAsnAspLysAsnGluValIleAlaAlaCysLeuLeuThrGluAla 60  
 Db 1492 ATTGTGGGAGTGAAGAATGATAAAATGAAGTTATAGCTGCATGTTTATTAAACAGAGGCA 1551

Qy 61 ArgIlePheLysPheTyrLysTyrPheTyrSerHisArgGlyProLeuLeuAspTyrPhe 80  
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Qy 81 AspAlaLysLeuValCysTyrPhePheLysGluLeuSerLysPheIleTyrLysAsnArg 100  
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Qy 101 GlyValPheIleLeuValAspProTyrLeuIleGluAsnLeuArgAspAlaAsnGlyArg 120  
 Db 1672 GGAGTATTATTCTTGATCCATATTAAATAGAGAATTAAAGAGATGCAAATGGTAGG 1731

Qy 121 IleIleLysAsnTyrAsnAsnSerValIleValLysMetLeuGlyLysIleGlyTyrLeu 140  
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Qy 161 AspLeuLysAspLysAspGluAsnGlnLeuLeuLysGluMetGluTyrGlnThrArgArg 180  
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Qy 181 AsnIleLysLysThrIleGluIleGlyValLysValGluAspLeuSerIleGluGluThr 200  
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Qy 201 AsnArgPheTyrLysLeuPheGlnMetAlaGluGluLysHisGlyPheHisPheMetAsn 220  
 Db 1972 AATCGATTAAATTGTTCAAATGGCTGAAGAAAACATGGTTTCATTTCATGAAT 2031

Qy 221 GluAspTyrPheLysArgMetGlnGluIleTyrLysAspLysAlaMetLeuLysIleAla 240  
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Qy 241 CysIleAsnLeuAsnGluTyrGlnAspLysLeuLysIleGlnLeuLeuLysIleGluAsn 260  
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Art Unit: 1652

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Db 2272 GAACTAATATTAGAAGATGGACCTGTTGGATTTAGCTGCTGCTTATTTATATGTACT 2331

Qy 321 AspAspGluValTyrTyrLeuSerSerGlySerAsnProLysTyrAsnGlnTyrMetGly 340  
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Art Unit: 1652

## APPENDIX B

Q9S685

ID Q9S685 PRELIMINARY; PRT; 414 AA.  
 AC Q9S685;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE FmhC.  
 GN FMHC.  
 OS *Staphylococcus aureus*.  
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.  
 OX NCBI\_TaxID=1280;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC55748;  
 RX MEDLINE=99177558; PubMed=10077832;  
 RA Tschierske M., Mori C., Rohrer S., Ehlert K., Shaw K.J.,  
 RA Berger-Bachi B.;  
 RT "Identification of three additional femAB-like open reading frames in  
 RT *Staphylococcus aureus*."  
 RL FEMS Microbiol. Lett. 171:97-102(1999).  
 DR EMBL; AF106851; AAD23963.1; -.  
 DR GO; GO:0009252; P:peptidoglycan biosynthesis; IEA.  
 DR InterPro; IPR003447; Meth resist.  
 DR Pfam; PF02388; FemAB; 1.  
 SQ SEQUENCE 414 AA; 49110 MW; 336D9BA80541E260 CRC64;

Query Match 100.0%; Score 2176; DB 2; Length 414;  
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 Db 361 NFYGITGVFSNEADDFGVQQFKKGNAHVEELIGDFIKPVRPILYKFAKLIYKV 414